

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: SAMSON, MICHEL
PARMENTIER, MARC
VASSART, GILBERT
LIBERT, FREDERICK

(ii) TITLE OF INVENTION: ACTIVE AND INACTIVE CC-CHEMOKINES RECEPTOR
AND NUCLEIC ACID MOLECULES ENCODING SAID RECEPTOR

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Knobbe, Martens, Olson & Bear
(B) STREET: 620 Newport Center Drive 16th Floor
(C) CITY: Newport Beach
(D) STATE: CA
(E) COUNTRY: U.S.A.
(F) ZIP: 92660

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/833,752
(B) FILING DATE: 9-APR-1997
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Altman, Daniel E
(B) REGISTRATION NUMBER: 34,115
(C) REFERENCE/DOCKET NUMBER:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 792 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 240..791

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTC	CCCC	AACAGAGCCA	AGCTCTCCAT	CTAGTGGACA	GGGAAGCTAG	CAGCAAACCT	60									
TCCCTT	CACT	ACAAA	ACTTC	ATTGCTTGGC	CAAAAAGAGA	GTTAATTCAA	TGTAGACATC	120								
TATGTAGGCA	ATTAAAAACC	TATTGATGTA	TAAAACAGTT	TGCATTTCATG	GAGGGCAACT		180									
AAATACATTC	TAGGACTTTA	TAAAAGATCA	CTTTTTATTT	ATGCACAGGG	TGGAACAAG		239									
ATG	GAT	TAT	CAA	GTG	TCA	AGT	CCA	ATC	TAT	GAC	ATC	AAT	TAT	TAT	ACA	287
Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	
1				5					10					15		
TCG	GAG	CCC	TGC	CAA	AAA	ATC	AAT	GTG	AAG	CAA	ATC	GCA	GCC	CGC	CTC	335
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	
			20					25				30				
CTG	CCT	CCG	CTC	TAC	TCA	CTG	GTG	TTC	ATC	TTT	GGT	TTT	GTG	GGC	AAC	383
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	
			35				40				45					
ATG	CTG	GTC	ATC	CTC	ATC	CTG	ATA	AAC	TGC	AAA	AGG	CTG	AAG	AGC	ATG	431
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	
			50				55				60					
ACT	GAC	ATC	TAC	CTG	CTC	AAC	CTG	GCC	ATC	TCT	GAC	CTG	TTT	TTC	CTT	479
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	
						70				75				80		
CTT	ACT	GTC	CCC	TTC	TGG	GCT	CAC	TAT	GCT	GCC	GCC	CAG	TGG	GAC	TTT	527
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	
				85				90				95				
GGA	AAT	ACA	ATG	TGT	CAA	CTC	TTG	ACA	GGG	CTC	TAT	TTT	ATA	GGC	TTC	575
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	
			100					105				110				
TTC	TCT	GGA	ATC	TTC	TTC	ATC	ATC	CTC	CTG	ACA	ATC	GAT	AGG	TAC	CTG	623
Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	
			115				120					125				
GCT	GTC	GTC	CAT	GCT	GTG	TTT	GCT	TTA	AAA	GCC	AGG	ACG	GTC	ACC	TTT	671
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	
			130				135				140					
GGG	GTG	GTG	ACA	AGT	GTG	ATC	ACT	TGG	GTG	GTG	GCT	GTG	TTT	GCG	TCT	719
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	
						150				155				160		
CTC	CCA	GGA	ATC	ATC	TTT	ACC	AGA	TCT	CAA	AAA	GAA	GGT	CTT	CAT	TAC	767
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	
				165				170					175			
ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	A								792
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr									
				180												

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 240..1295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT	60
TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TG TAGACATC	120
TATGTAGGCA ATTAAAAACC TATTGATGTA TAAACAGTT TGCATTCATG GAGGGCAACT	180
AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGAACAAG	239
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
1 5 10 15	
TGG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
20 25 30	
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
35 40 45	
ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
50 55 60	
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
65 70 75 80	
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
85 90 95	
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
100 105 110	
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120 125	
GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
130 135 140	
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT	719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
145 150 155 160	
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
165 170 175	

ACC	TGC	AGC	TCT	CAT	TTT	CCA	TAC	AGT	CAG	TAT	CAA	TTC	TGG	AAG	AAT	815
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	
			180					185					190			
TTC	CAG	ACA	TTA	AAG	ATA	GTC	ATC	TTG	GGG	CTG	GTC	CTG	CCG	CTG	CTT	863
Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	
		195					200					205				
GTC	ATG	GTC	ATC	TGC	TAC	TCG	GGA	ATC	CTA	AAA	ACT	CTG	CTT	CGG	TGT	911
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	
	210					215					220					
CGA	AAT	GAG	AAG	AAG	AGG	CAC	AGG	GCT	GTG	AGG	CTT	ATC	TTC	ACC	ATC	959
Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile	
225					230					235					240	
ATG	ATT	GTT	TAT	TTT	CTC	TTC	TGG	GCT	CCC	TAC	AAC	ATT	GTC	CTT	CTC	1007
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu	
			245					250					255			
CTG	AAC	ACC	TTC	CAG	GAA	TTC	TTT	GGC	CTG	AAT	AAT	TGC	AGT	AGC	TCT	1055
Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser	
		260						265				270				
AAC	AGG	TTG	GAC	CAA	GCT	ATG	CAG	GTG	ACA	GAG	ACT	CTT	GGG	ATG	ACG	1103
Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	
	275						280				285					
CAC	TGC	TGC	ATC	AAC	CCC	ATC	ATC	TAT	GCC	TTT	GTC	GGG	GAG	AAG	TTC	1151
His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	
	290					295					300					
AGA	AAC	TAC	CTC	TTA	GTC	TTC	TTC	CAA	AAG	CAC	ATT	GCC	AAA	CGC	TTC	1199
Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	Ile	Ala	Lys	Arg	Phe	
305					310					315					320	
TGG	AAA	TGC	TGT	TCT	ATT	TTC	CAG	CAA	GAG	GCT	CCC	GAG	CGA	GCA	AGC	1247
Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser	
			325					330					335			
TCA	GTT	TAC	ACC	CGA	TCC	ACT	GGG	GAG	CAG	GAA	ATA	TCT	GTG	GGC	TTG	1295
Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	Val	Gly	Leu	
			340				345						350			
TGACACGGAC	TCAAGTGGGC	TGGTGACCCA	GTCAGAGTTG	TGCACATGGC	TTAGTTTTCA											1355
TACACAGCCT	GGGCTGGGGG	TNGGTTGGNN	GAGGTCTTTT	TTAAAAGGAA	GTTACTGTTA											1415
TAGAGGGTCT	AAGATTCATC	CATTTATTTG	GCATCTGTTT	AAAGTAGATT	AGATCCGAAT											1475
TC																1477

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 240..884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAATTCCCCC AACAGAGCCA AGCTCTCCAT CTAGTGGACA GGGAAGCTAG CAGCAAACCT	60
TCCCTTCACT ACAAACCTTC ATTGCTTGGC CAAAAAGAGA GTTAATTCAA TGTAGACATC	120
TATGTAGGCA ATTAAAAACC TATTGATGTA TAAAACAGTT TGCATTCATG GAGGGCAACT	180
AAATACATTC TAGGACTTTA TAAAAGATCA CTTTTTATTT ATGCACAGGG TGGACAAG	239
ATG GAT TAT CAA GTG TCA AGT CCA ATC TAT GAC ATC AAT TAT TAT ACA	287
Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr	
1 5 10 15	
TCG GAG CCC TGC CAA AAA ATC AAT GTG AAG CAA ATC GCA GCC CGC CTC	335
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu	
20 25 30	
CTG CCT CCG CTC TAC TCA CTG GTG TTC ATC TTT GGT TTT GTG GGC AAC	383
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn	
35 40 45	
ATG CTG GTC ATC CTC ATC CTG ATA AAC TGC AAA AGG CTG AAG AGC ATG	431
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met	
50 55 60	
ACT GAC ATC TAC CTG CTC AAC CTG GCC ATC TCT GAC CTG TTT TTC CTT	479
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu	
65 70 75 80	
CTT ACT GTC CCC TTC TGG GCT CAC TAT GCT GCC GCC CAG TGG GAC TTT	527
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe	
85 90 95	
GGA AAT ACA ATG TGT CAA CTC TTG ACA GGG CTC TAT TTT ATA GGC TTC	575
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe	
100 105 110	
TTC TCT GGA ATC TTC TTC ATC ATC CTC CTG ACA ATC GAT AGG TAC CTG	623
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu	
115 120 125	
GCT GTC GTC CAT GCT GTG TTT GCT TTA AAA GCC AGG ACG GTC ACC TTT	671
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe	
130 135 140	
GGG GTG GTG ACA AGT GTG ATC ACT TGG GTG GTG GCT GTG TTT GCG TCT	719
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser	
145 150 155 160	
CTC CCA GGA ATC ATC TTT ACC AGA TCT CAA AAA GAA GGT CTT CAT TAC	767
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr	
165 170 175	
ACC TGC AGC TCT CAT TTT CCA TAC ATT AAA GAT AGT CAT CTT GGG GCT	815
Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala	
180 185 190	
GGT CCT GCC GCT GCT TGT CAT GGT CAT CTG CTA CTC GGG AAT CCT AAA	863
Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys	
195 200 205	
AAC TCT GCT TCG GTG TCG AAA TGAGAAGAAG AGGCACAGGG CTGTGAGGCT	914
Asn Ser Ala Ser Val Ser Lys	
210 215	
TATCTTCACC ATCATGATTG TTTATTTTCT CTTCTGGGCT CCCTACAACA TTGTCCTTCT	974

CCTGAACACC	TTCCAGGAAT	TCTTTGGCCT	GAATAATTGC	AGTAGCTCTA	ACAGGTTGGA	1034
CCAAGCTATG	CAGGTGACAG	AGACTCTTGG	GATGACGCAC	TGCTGCATCA	ACCCCATCAT	1094
CTATGCCTTT	GTCGGGGAGA	AGTTCAGAAA	CTACCTCTTA	GTCTTCTTCC	AAAAGCACAT	1154
TGCCAAACGC	TTCTGCAAAT	GCTGTTCTAT	TTTCCAGCAA	GAGGCTCCCG	AGCGAGCAAG	1214
CTCAGTTTAC	ACCCGATCCA	CTGGGGAGCA	GGAAATATCT	GTGGGCTTGT	GACACGGACT	1274
CAAGTGGGCT	GGTGACCCAG	TCAGAGTTGT	GCACATGGCT	TAGTTTTCAT	ACACAGCCTG	1334
GGCTGGGGGT	GGTTGGGAGG	TCTTTTTTAA	AAGGAAGTTA	CTGTTATAGA	GGGTCTAAGA	1394
TTCATCCATT	TATTTGGCAT	CTGTTTAAAG	TAGATTAGAT	CCGAATTC		1442

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	1	5	10	15
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	20	25	30	
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	35	40	45	
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	50	55	60	
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	65	70	75	80
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	85	90	95	
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	100	105	110	
Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	115	120	125	
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	130	135	140	
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	145	150	155	160
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	165	170	175	
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr									180			

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met	Asp	Tyr	Gln	Val	Ser	Ser	Pro	Ile	Tyr	Asp	Ile	Asn	Tyr	Tyr	Thr	1	5	10	15
Ser	Glu	Pro	Cys	Gln	Lys	Ile	Asn	Val	Lys	Gln	Ile	Ala	Ala	Arg	Leu	20	25	30	
Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	35	40	45	
Met	Leu	Val	Ile	Leu	Ile	Leu	Ile	Asn	Cys	Lys	Arg	Leu	Lys	Ser	Met	50	55	60	
Thr	Asp	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Phe	Phe	Leu	65	70	75	80
Leu	Thr	Val	Pro	Phe	Trp	Ala	His	Tyr	Ala	Ala	Ala	Gln	Trp	Asp	Phe	85	90	95	
Gly	Asn	Thr	Met	Cys	Gln	Leu	Leu	Thr	Gly	Leu	Tyr	Phe	Ile	Gly	Phe	100	105	110	
Phe	Ser	Gly	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	115	120	125	
Ala	Val	Val	His	Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	130	135	140	
Gly	Val	Val	Thr	Ser	Val	Ile	Thr	Trp	Val	Val	Ala	Val	Phe	Ala	Ser	145	150	155	160
Leu	Pro	Gly	Ile	Ile	Phe	Thr	Arg	Ser	Gln	Lys	Glu	Gly	Leu	His	Tyr	165	170	175	
Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn	180	185	190	
Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	195	200	205	
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	210	215	220	
Arg	Asn	Glu	Lys	Lys	Arg	His	Arg	Ala	Val	Arg	Leu	Ile	Phe	Thr	Ile	225	230	235	240
Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp	Ala	Pro	Tyr	Asn	Ile	Val	Leu	Leu	245	250	255	
Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe	Gly	Leu	Asn	Asn	Cys	Ser	Ser	Ser	260	265	270	
Asn	Arg	Leu	Asp	Gln	Ala	Met	Gln	Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	275	280	285	
His	Cys	Cys	Ile	Asn	Pro	Ile	Ile	Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	290	295	300	
Arg	Asn	Tyr	Leu	Leu	Val	Phe	Phe	Gln	Lys	His	Ile	Ala	Lys	Arg	Phe	305	310	315	320
Cys	Lys	Cys	Cys	Ser	Ile	Phe	Gln	Gln	Glu	Ala	Pro	Glu	Arg	Ala	Ser	325	330	335	
Ser	Val	Tyr	Thr	Arg	Ser	Thr	Gly	Glu	Gln	Glu	Ile	Ser	Val	Gly	Leu	340	345	350	

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Met Asp Tyr Gln Val Ser Ser Pro Ile Tyr Asp Ile Asn Tyr Tyr Thr
 1          5          10          15
Ser Glu Pro Cys Gln Lys Ile Asn Val Lys Gln Ile Ala Ala Arg Leu
          20          25          30
Leu Pro Pro Leu Tyr Ser Leu Val Phe Ile Phe Gly Phe Val Gly Asn
          35          40          45
Met Leu Val Ile Leu Ile Leu Ile Asn Cys Lys Arg Leu Lys Ser Met
 50          55          60
Thr Asp Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp Leu Phe Phe Leu
65          70          75          80
Leu Thr Val Pro Phe Trp Ala His Tyr Ala Ala Ala Gln Trp Asp Phe
          85          90          95
Gly Asn Thr Met Cys Gln Leu Leu Thr Gly Leu Tyr Phe Ile Gly Phe
          100          105          110
Phe Ser Gly Ile Phe Phe Ile Ile Leu Leu Thr Ile Asp Arg Tyr Leu
          115          120          125
Ala Val Val His Ala Val Phe Ala Leu Lys Ala Arg Thr Val Thr Phe
130          135          140
Gly Val Val Thr Ser Val Ile Thr Trp Val Val Ala Val Phe Ala Ser
145          150          155          160
Leu Pro Gly Ile Ile Phe Thr Arg Ser Gln Lys Glu Gly Leu His Tyr
          165          170          175
Thr Cys Ser Ser His Phe Pro Tyr Ile Lys Asp Ser His Leu Gly Ala
          180          185          190
Gly Pro Ala Ala Ala Cys His Gly His Leu Leu Leu Gly Asn Pro Lys
          195          200          205
Asn Ser Ala Ser Val Ser Lys
210          215

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Leu	Ser	Thr	Ser	Arg	Ser	Arg	Phe	Ile	Arg	Asn	Thr	Asn	Glu	Ser
1				5					10					15	
Gly	Glu	Glu	Val	Thr	Thr	Phe	Phe	Asp	Tyr	Asp	Tyr	Gly	Ala	Pro	Cys
			20					25					30		
His	Lys	Phe	Asp	Val	Lys	Gln	Ile	Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu
		35				40					45				
Tyr	Ser	Leu	Val	Phe	Ile	Phe	Gly	Phe	Val	Gly	Asn	Met	Leu	Val	Val
	50					55					60				
Leu	Ile	Leu	Ile	Asn	Cys	Lys	Lys	Leu	Lys	Cys	Leu	Thr	Asp	Ile	Tyr
65				70						75				80	
Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Ile	Ile	Thr	Leu	Pro
				85					90					95	
Leu	Trp	Ala	His	Ser	Ala	Ala	Asn	Glu	Trp	Val	Phe	Gly	Asn	Ala	Met
			100					105					110		
Cys	Lys	Leu	Phe	Thr	Gly	Leu	Tyr	His	Ile	Gly	Tyr	Phe	Gly	Gly	Ile
		115					120					125			
Phe	Phe	Ile	Ile	Leu	Leu	Thr	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His
	130					135					140				
Ala	Val	Phe	Ala	Leu	Lys	Ala	Arg	Thr	Val	Thr	Phe	Gly	Val	Val	Thr
145					150					155					160
Ser	Val	Ile	Thr	Trp	Leu	Val	Ala	Val	Phe	Ala	Ser	Val	Pro	Gly	Ile
				165					170					175	
Ile	Phe	Thr	Lys	Cys	Gln	Lys	Glu	Asp	Ser	Val	Tyr	Val	Cys	Gly	Pro
			180					185					190		
Tyr	Phe	Pro	Arg	Gly	Trp	Asn	Asn	Phe	His	Thr	Ile	Met	Arg	Asn	Ile
		195				200						205			
Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu	Ile	Met	Val	Ile	Cys	Tyr	Ser	Gly
	210					215					220				
Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys	Arg	Asn	Glu	Lys	Lys	Arg	His	Arg
225				230						235					240
Ala	Val	Arg	Val	Ile	Phe	Thr	Ile	Met	Ile	Val	Tyr	Phe	Leu	Phe	Trp
				245					250					255	
Thr	Pro	Tyr	Asn	Ile	Val	Ile	Leu	Leu	Asn	Thr	Phe	Gln	Glu	Phe	Phe
			260					265					270		
Gly	Leu	Ser	Asn	Cys	Glu	Ser	Thr	Ser	Gln	Leu	Asp	Gln	Ala	Ile	Gln
		275					280					285			
Val	Thr	Glu	Thr	Leu	Gly	Met	Thr	His	Cys	Cys	Ile	Asn	Pro	Ile	Ile
	290					295					300				
Tyr	Ala	Phe	Val	Gly	Glu	Lys	Phe	Arg	Arg	Tyr	Ile	Ser	Val	Phe	Phe
305					310					315					320
Arg	Lys	His	Ile	Xaa	Xaa	Xaa	Phe	Cys	Lys	Gln	Cys	Pro	Val	Phe	Tyr
				325					330					335	
Arg	Glu	Thr	Val	Asp	Gly	Val	Thr	Ser	Thr	Asn	Thr	Pro	Ser	Thr	Gly
			340					345					350		
Glu	Gln	Glu	Val	Ser	Ala	Gly	Leu								
		355					360								

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

[illegible]

355

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Glu	Thr	Pro	Asn	Thr	Thr	Glu	Asp	Tyr	Asp	Thr	Thr	Thr	Glu	Phe
1				5					10					15	
Asp	Tyr	Gly	Asp	Ala	Thr	Pro	Cys	Gln	Lys	Val	Asn	Glu	Arg	Ala	Phe
			20					25					30		
Gly	Ala	Gln	Leu	Leu	Pro	Pro	Leu	Tyr	Ser	Leu	Val	Phe	Val	Ile	Gly
		35					40					45			
Leu	Val	Gly	Asn	Ile	Leu	Val	Val	Leu	Val	Leu	Val	Gln	Tyr	Lys	Arg
		50				55					60				
Leu	Lys	Asn	Met	Thr	Ser	Ile	Tyr	Leu	Leu	Asn	Leu	Ala	Ile	Ser	Asp
65					70					75				80	
Leu	Leu	Phe	Ile	Phe	Thr	Leu	Pro	Phe	Trp	Ile	Asp	Tyr	Lys	Leu	Lys
				85					90					95	
Asp	Asp	Trp	Val	Phe	Gly	Asp	Ala	Met	Cys	Lys	Ile	Ile	Ser	Gly	Phe
			100					105					110		
Tyr	Tyr	Thr	Gly	Leu	Tyr	Ser	Glu	Ile	Phe	Phe	Ile	Ile	Leu	Leu	Thr
		115					120					125			
Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Phe	Ala	Ile	Arg	Ala
		130				135					140				
Arg	Thr	Val	Thr	Phe	Gly	Val	Ile	Thr	Ser	Ile	Ile	Ile	Trp	Ala	Ile
145					150					155				160	
Ala	Ile	Ile	Ala	Ser	Met	Pro	Gly	Leu	Tyr	Phe	Ser	Lys	Thr	Gln	Trp
				165					170					175	
Glu	Phe	Thr	His	His	Thr	Cys	Ser	Leu	His	Phe	Pro	His	Glu	Ser	Leu
			180					185					190		
Arg	Glu	Trp	Lys	Leu	Phe	Gln	Ala	Leu	Lys	Leu	Asn	Leu	Phe	Gly	Leu
		195					200					205			
Val	Leu	Pro	Leu	Leu	Val	Met	Ile	Ile	Cys	Tyr	Ile	Gly	Ile	Ile	Lys
		210				215					220				
Ile	Leu	Leu	Arg	Arg	Pro	Asn	Glu	Lys	Lys	Ser	Lys	Ala	Val	Arg	Leu
225					230					235				240	
Ile	Phe	Val	Ile	Met	Ile	Ile	Phe	Phe	Leu	Phe	Trp	Ile	Pro	Tyr	Asn
				245					250					255	
Leu	Thr	Ile	Ile	Ile	Ser	Val	Phe	Gln	Asp	Phe	Leu	Phe	Thr	His	Glu
			260					265					270		
Cys	Glu	Gln	Ser	Arg	His	Leu	Asp	Leu	Ala	Val	Gln	Val	Thr	Glu	Val
		275					280					285			
Ile	Ala	Tyr	Thr	His	Cys	Cys	Val	Asn	Glu	Val	Ile	Tyr	Ala	Phe	Val
		290				295						300			

Gly	Glu	Arg	Phe	Arg	Lys	Tyr	Ile	Arg	Gln	Leu	Glu	His	Arg	Arg	Val
305					310					315					320
Ala	Val	His	Leu	Val	Lys	Trp	Leu	Pro	Phe	Leu	Ser	Val	Asp	Arg	Ile
			325						330					335	
Glu	Arg	Val	Ser	Ser	Thr	Ser	Pro	Ser	Thr	Gly	Glu	His	Glu	Ile	Ser
			340					345					350		
Ala	Gly	Phe													
		355													

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Asn	Pro	Thr	Asp	Ile	Ala	Asp	Thr	Thr	Leu	Asp	Glu	Ser	Ile	Tyr
			5					10						15	
Ser	Asn	Tyr	Tyr	Leu	Tyr	Glu	Ser	Ile	Pro	Lys	Pro	Cys	Thr	Lys	Glu
		20					25						30		
Gly	Ile	Lys	Ala	Phe	Gly	Glu	Leu	Phe	Leu	Pro	Pro	Leu	Tyr	Ser	Leu
		35				40						45			
Val	Glu	Val	Phe	Gly	Leu	Ile	Gly	Asn	Ser	Val	Val	Val	Leu	Val	Leu
	50				55					60					
Phe	Lys	Tyr	Lys	Arg	Ile	Arg	Ser	Met	Thr	Asp	Val	Tyr	Leu	Leu	Asn
				70					75					80	
Leu	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Val	Phe	Ser	Leu	Pro	Phe	Trp	Gly
			85					90					95		
Tyr	Tyr	Ala	Ala	Asp	Gln	Trp	Val	Phe	Gly	Leu	Gly	Ile	Cys	Lys	Met
		100					105					110			
Ile	Ser	Trp	Met	Tyr	Leu	Val	Gly	Phe	Tyr	Ser	Gly	Ile	Phe	Phe	Val
		115				120					125				
Met	Ile	Met	Ser	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Ala	Val	Glu
	130				135					140					
Xaa	Xaa	Xaa	Ala	Arg	Thr	Ile	Ile	Tyr	Gly	Val	Ile	Thr	Ser	Leu	Ala
145				150					155					160	
Thr	Trp	Ser	Val	Ala	Val	Phe	Ala	Ser	Leu	Pro	Gly	Phe	Ile	Phe	Ser
			165					170					175		
Thr	Cys	Tyr	Thr	Glu	Arg	Asn	His	Thr	Tyr	Cys	Lys	Thr	Lys	Tyr	Ser
		180					185					190			
Leu	Asn	Ser	Thr	Thr	Trp	Lys	Val	Leu	Ser	Ser	Leu	Glu	Ile	Asn	Ile
		195				200					205				
Leu	Gly	Leu	Val	Ile	Pro	Leu	Gly	Ile	Met	Leu	Phe	Cys	Tyr	Ser	Met
	210					215				220					
Ile	Ile	Arg	Thr	Leu	Gln	His	Cys	Lys	Asn	Glu	Lys	Lys	Asn	Lys	Ala
225				230					235					240	
Val	Lys	Met	Ile	Phe	Ala	Val	Val	Val	Leu	Phe	Leu	Gly	Phe	Trp	Thr

Pro	Tyr	Asn	Ile	Val	Leu	Phe	Leu	Glu	Thr	Leu	Val	Glu	Leu	Glu	Val
			245					250					255		
Ile	Gln	Asp	Cys	Thr	Phe	Glu	Arg	Tyr	Leu	Asp	Tyr	Ala	Ile	Gln	Ala
		260						265					270		
Thr	Glu	Thr	Leu	Ala	Phe	Val	His	Cys	Cys	Leu	Asn	Pro	Ile	Ile	Tyr
		275						280					285		
Phe	Phe	Leu	Gly	Glu	Lys	Phe	Arg	Lys	Tyr	Ile	Ile	Gln	Leu	Phe	Lys
305					310					315					320
Xaa	Xaa	Xaa	Gly	Leu	Phe	Val	Ile	Cys	Gln	Tyr	Cys	Gly	Leu	Leu	Gln
			325						330						335
Ile	Tyr	Ser	Ala	Asp	Thr	Pro	Ser	Ser	Ser	Tyr	Thr	Gln	Ser	Thr	Met
			340					345					350		
Asp	His	Asp	Leu	His	Asp	Ala	Leu								
		355					360								

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr	Cys	Ser	Ser	His	Phe	Pro	Tyr	Ser	Gln	Tyr	Gln	Phe	Trp	Lys	Asn
				5					10					15	
Phe	Gln	Thr	Leu	Lys	Ile	Val	Ile	Leu	Gly	Leu	Val	Leu	Pro	Leu	Leu
			20					25					30		
Val	Met	Val	Ile	Cys	Tyr	Ser	Gly	Ile	Leu	Lys	Thr	Leu	Leu	Arg	Cys
		35					40					45			
Arg	Asn	Glu	Lys	Lys	Arg										
50															

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTCCATACA	GTCAGTATCA	ATTCTGGAAG	AATTTCCAGA	CATTAAAGAT	AGTCATCTTG	60
GGGCTGGTCC	TGCCGCTGCT	TGTCATGGTC	ATCTGCTACT	CGGGAATCCT	AAAAACTCTG	120
CTTCGGTGTG	GAAATGAGAA	GAAGAGG				147

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Phe	Pro	Tyr	Ile	Lys	Asp	Ser	His	Leu	Gly	Ala	Gly	Pro	Ala	Ala	Ala
1				5				10						15	
Cys	His	Gly	His	Leu	Leu	Leu	Gly	Asn	Pro	Lys	Asn	Ser	Ala	Ser	Val
			20					25					30		
Ser	Lys														

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TCGAGGATCC AAGATGGATT ATCAAGT

27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CTGATCTAGA GCCATGTGCA CAACTCT

27

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCTGGCTGTC GTCCATGCTG

20

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGATCTAGA GCCATGTGCA CAACTCT

27

CTGATCTAGA GCCATGTGCA CAACTCT